Uncharted territory: Exploring life in Yellowstone National Park's hot springs

by Ann Rodman and Kendra Maas

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Biological Science Technician Kendra Maas samples hot water organisms in Yellowstone National Park. Adapted to extreme environments, filamentous bacteria (inset, top), layered bacterial mats (inset, bottom), and other microbes are virtually unexplored in the park. The inventory will help protect this valuable resource and improve our understanding of these amazing and potentially beneficial organisms.

YELLOWSTONE NATIONAL PARK IS HOME TO THE most varied and largest intact geothermal area in the world. High-temperature natural systems comprising spectacular geysers, hot springs, mud pots, and steam vents include a virtually unexplored wealth of living organisms that have the potential for remarkable scientific, social, and economic benefits. In 2002, with funding from the Natural Resource Challenge through the NPS Biological Resources Management Division, Yellowstone embarked on a collaborative, multiyear research effort with Portland State University and the University of New Mexico to create a baseline inventory of the microbial communities in geothermal areas throughout the park.

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Yellowstone National Park has been inventorying the chemical and physical characteristics of its geothermal ecosystems for years; however, very little is known about the biodiversity, ecology, and distribution of the thermophiles within these systems. Thermophiles are microorganisms that thrive in high temperatures and, in Yellowstone National Park, extremes of pH. In 1996 the list of thermophiles in the park included only 35 species. Park staff searched the scientific literature in 2000 and 2001 for information about park thermophiles. Documented in the literature were 406 organisms from 105 different pools, meaning that fewer than 1% of the park's hot springs have been studied for thermophiles!

Research efforts got under way to correct this gap in spring 2002. The research team began by testing collection protocols and refining laboratory techniques using 18 samples taken from park thermal areas. Until the early 1990s, measurement of microbial species diversity was restricted to the small (<1%) portion of microorganisms that could be grown in petri dishes. This limitation has been partially alleviated by the development of molecular techniques based on gene sequences in small pieces of ribosomal RNA that allow for the characterization of microorganisms without the need to grow them in the laboratory.

The 18 samples were analyzed to reveal 71 unique gene sequences. Each gene sequence represents a distinct organism. These sequences were then compared with all sequences listed in GenBank, a large database of gene sequences hosted by the National Institutes of Health. Fifty-eight of the 71 sequences matched a known organism in GenBank. Some of the remaining 13 sequences will represent previously unknown organisms.

In summer 2002 the research team chose 300 sampling locations from a database of 6,500 possible sites. The sampling sites represent the full range of pH and temperature combinations found in the park. From June to September the team collected 216 samples from 5 of the park's 12 major thermal areas. Digital photographs and biomass samples were taken at each site in addition to readings of pH, temperature, and precise location. Samples showed a wide variation in pH levels, from 1.7 to 9.3. In the fall the ribosomal RNA was extracted and analyzed from 80 of the 216 samples. The results will set priorities for sampling during summer 2003.

The process of inventorying the biological characteristics of Yellowstone National Park's thermal areas is crucial to developing a thorough understanding of the kinds of organisms that live in these high-temperature systems and how they change over time. Good science will allow park managers to identify and address threats that can alter these ecosystems and change the composition of microbial communities, including low aquifer recharge rates, landslides, floods, energy development, and visitor impacts. Until a baseline inventory is accomplished, some amazing, and potentially beneficial, organisms will have incomplete protection simply because their existence is not known. ■

ann_rodman@nps.gov
Supervisory GIS Specialist, Yellowstone National Park, Wyoming

kendra_maas@nps.gov
Biological Science Technician, Yellowstone National Park, Wyoming